```
ggcacgaggcgccGGGCCATGGgcCTCGAGcCCGCCGGA-CCCCCGCGAGCCCGCTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 CTGCGGCGTGACTGGAGGCCCAGATGGTCATGGGCCCAGTGCTACTACAACGAGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGCGGCGTGACTGGAGGCCCAGATGGTCATCATGGGCCAGTGCTACTACAACGAGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTCGTGGTGGCACTGGGGCTGACCGTCAGCGTGCTGGTGCTGCTGACCAATCTGCTGGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTCGTGGTGGCACTGGGGCTGACCGTCAGCGTGCTGGTGCTGCTGACCAATCTGCTGGTCA
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    Multiple Sequence Alignment Program

                                                                                                                                                                                                                                                                                                                                                                                                 Region Alignment: (listed in Clustered order)
                                                                                                                                                                                                                                                                                                                   selected sequences:
                                                                                                                                                                                                                                                                                                                                             (1-375)
(1-1734)
                                                                                                                                              Identity
                                                                                                                                                                                                                                     5.00
                                                                                                                                                                                                                                                              1.00
                                                                                                                                                                      OffOffOff
                                                                                       Thu 21 Feb 102 14:55:14-PST
                                                                                                                                                                                                                      AMINO-Res-length = 2

DELetion-weight = 5

LEngth-factor = 0

Matching-weight = 1

NUCLEIC-Res-length = 4

SPread-factor = 5(
                                                                                                                                                                                                                                                                                                                                                         -752D-2
                                                                                                                                          Nucleic Alphabet
Output line length
Compress
             IntelliGenetics
                                                                                                                 Solution Parameters:
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                                                                                                                                                                                               Randomization
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                                                              Release 5.4
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0
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aa419064 US-09-274-	350	CGCACAGCCCGACTTTCACTTGAGGG
consensus		CGCACAGCCCGACTTTCACTTGAGGGctggttcctgcggcagggcttgctggacacaagcc
aa419064	376	
US-09-274-	428	tcactgcgtcggtggccacactgctggccatcgccgtggagctgcaccgcagtgtgatgtc
consensus		tcactgcgtcggtggccacactgctggccatcgccgtggagctgcaccgcagtgtgatgtc
aa419064	376	
US-09-274-	489	cgigoagoigocagocoigocogiggocgogiggicaigoicaiigigggogigigg
consensus		cgigcagcigcacagccgcctgccccgtggccgcgtggtcatgcicattgtgggcgtgigg
aa419064	376	
US-09-274-	550	giggetgocetgggetggetgetgeetgeceactectggeactgeetetgigeetgg
consensus	_	$\mathfrak{gtggctgcctgggctgctgcctgcccactcctggcactgcctctgtgccctgg}$
aa419064	376	
US-09-274-	611	${\tt accgctgctcacgcatggcaccctgctcagccgctcctatttggccgtctgggctctgtc}$
consensus		accgctgctcacgcatggcaccctgctcagccgctcctatttggccgtctgggctctgtc
aa419064	376	
US-09-274-	672	gagectgtctgtttcctgctcatggtggctgtgtacacccgcattttcttctacgtgcgg
consensus		gagectgtetgtetteetgeteatggtggetgtgtacaecegeattttettetaegtgegg
aa419064	376	
US-09-274-	733	cggcgagtgcagcgcatggcagagcatgtcagctgccacccccgctaccgagagaccacgc
consensus		cggcgagtgcagcgtatggcagagcatgtcagctgccaccccgctaccgagagaccacgc
aa419064	376	
US-09-274-	794	${\tt tcagcctggtcaagactgttgtcatcatcctgggggggttcgtggtctgctggacaccagg}$
consensus	-	tcagcctggtcaagactgttgtcatcatcctgggggcgttcgtggtctgctggacaccagg
aa419064	376	
US-09-274-	855	ccaggiggiacigcicciggaiggittaggcigigagiccigcaaigicciggcigiagaa
consensus	Ü	ccaggiggiacigcicciggaiggitiaggcigigagiccigcaaigicciggcigiagaa
aa419064	376	
US-09-274-	916 a	agtacttcctactgttggccgaggccaactcactggtcaatgctgctgtgtactcttgcc
consensus	10	aagtacttoctactgttggccgaggccaactcactggtcaatgctgctgtgtactcttgcc

aa419064 376

consensus

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Multiple Sequence Alignment Program
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    = Identity
n = 80
= Off
= Off
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1.1.1
1.00
5.00
                                                                                                                                                                                                                                                                                                                                                                                                                                      Thu 21 Feb 102 14:54:03-PST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMINO.Res.length = DELotion.weight | LEngth.factor = Matching-weight | YCLEIC-Res.length = read-factor = Ength = read-factor | Ength = Ength =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Output line length
> 0 < 01 | 0 IntelliGenetics > 0 <
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Randomization
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MVIMGQCYYNETIGFFYNNSGKELSSHWRPKDVVVVALGLIVSVLVLLINLLVIAAIASNR Region Alignment: (listed in Clustered order) HARRIS-EDG US-09-274consensus

RFHQPIYYLLGNLAAADLFAGVAYLFLMFHTGPRTARLSLEGWFLRQGLLDTSLTASVATL US-09-274-HARRIS-EDG US-09-274consensus HARRIS-EDG

LAIAVERHRSVMAVQLHSRLPRGRVVMLIVGVWVAALGLGLLPAHSWHCLCALDRCSRMAP LLSRSYLAVWALSSLLVFLLMVAVYTRIFFYVRRRVQSMAEHVSCHPRYRETTLSLVKTVV 184 HARRIS-EDG ensue

245 IILGAFVVCWTPGQVVLLLDGLGCESCNVLAVEKYFLLLAEANSLVNAAVYSCRDAEMRRT IILGAFVVCWTPGQVVLLLDGLGCESCNVLAVEKYFLLLAEANSLVNAAVYSCRD-EMRRT HARRIS-EDG US-09-274-HARRIS-EDG consensus

FRRLLCCACLRQSTRESVHYTSSAQGGASTRIMLPENGHPLMTPPFSYLELQRYAASNKST FRRLLCCACLRQSTRESVHYTSSAQGGASTRIMLPENGHPLMTPPFSYLELQRYAASNKST

306

US-09-274-

consensus

LLSRSYLAVWALSSLLVFLLMVAVYTRIFFYVRRRVQ-MAEHVSCHPRYRETTLSLVKTVV

184

US-09-274-

consensus

367 APDDLWVLLAQPNQQD 367 APDDLWVLLAQPNQQD APDDLWVLLAQPNQQD HARRIS-EDG US-09-274consensus

Alignment score = 380.00

Scoring matrix:

380